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a multi-chambered digestive system to host a complex microbial community that can break down the lignocellulosic material they feed on. There are both core and transitory species that can change with diet and animal condition over the course of a single day. Approaches based on identification of the OTU have several limitations, such as the number of the unknown species that colonise the environment, the difficulty to characterise their metabolic pathways and their mutual interactions. We took a different approach that aims to be used in studying the relationship in the community and to understand the patterns of the interactions between the organisms. We developed a framework that can be used in a number of different studies, without knowing a prior knowledge of the organisms that compose the community, taking a functional approach at the analysis, using evolutionary rates as the guide to understand the microbial ecosystem analysed. The framework has been used to study the microbial community found in the rumen of 14 tube sampled Holstein-Friesian cattles as a test for the framework and work is underway to study the differences in the microbial communities that colonise the solid and liquid phases that are present in the rumen.

Systems biology approach for the identification of genetic determinants of colony morphology switch in natural *S. cerevisiae* strain

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Colony morphology is a fascinating phenotype described in unicellular organisms as a possible step towards multicellularity. The spreading of filamentous structures is used by some pathogenic fungi, as *Candida albicans*, to invade human tissues thus causing infection. This phenotype, rarely observed in *Saccharomyces cerevisiae* colonies, is present in heterozygosis in the M28 *S. cerevisiae* strain, isolated from damaged grapes of the Montalcino area (Italy). Meiotic segregants of M28 show mendelian inheritance of colony morphology, thus making this strain the best suitable model to study the genetic determinants of structured colonies (filigreed). We analyzed cellular and colony morphology of M28 meiotic segregants in several different carbon sources. The addition of ethanol as the only carbon source lead to an increase in filamentation: in this perspective the stable and uniform morphotype, induced by ethanol, could reflect an adaptation to stress. In order to investigate the correlation between invasiveness, filamentous morphotype and pseudohyphal growth in *S. Cerevisiae,* we assessed the ability of this natural strain to invade solid media. Transcriptional analysis by means of microarrays on cells grown in fermentable and not-fermentable carbon sources and Functional Enrichment Analysis identified the genes involved in the regulation of colony morphogenesis. Our results support the hypothesis of an ecological function of filamentous phenotype in creating a community adaptable to the shifts of the environmental conditions. Whole genome comparative analysis on 12 M28 sporal derivatives of three different tetrads, with Next-Generation Sequencing (NGS) approach, allowed to discover mutations in genes candidate to be the genetic determinants of the colony morphology phenotype. We demonstrate that a number of three tetrads is sufficient to map a genetic trait with mendelian inheritance. RNA-seq based transcriptomics on the all M28 sequenced genome allowed to identify a gene expression profile associated to the filamentous morphotype and to confirm the candidate morphogenesis regulatory genes.

Drosophila population genomics

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The analysis of next generation sequencing data from pooled individuals (Pool-Seq) is a cost effective approach to study allele frequency changes in natural and experimental populations. I will provide some case studies in *Drosophila* demonstrating the power and limitations of Pool-Seq.